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(54) **Novel Phytase**

(57) A novel phytase is disclosed. The phytase consists essentially of a single type of subunits, and can hydrolyze a phytate to myo-inositol. A gene encoding the phytase, which is originated from *Schwanniomyces occidentalis* is also disclosed.

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Description

BACKGROUND OF THE INVENTION

5 I. Field of the Invention

The present invention relates to a novel phytase, a gene encoding the same, a recombinant vector containing the gene, a microorganism transformed with the recombinant vector, and a method for converting a phytate into *myo*-inositol using the phytase produced by the transformant.

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II. Description of the Related Art

Phytase is a phosphatase which dephosphorylates phytic acid. The phytase which hydrolyzes the phosphate at 6-position is called 6-phytase (EC. 3.1.3.2.6.) and the phytase which hydrolyzes the phosphate at 3-position is called 3-phytase (EC. 3.1.3.8.). The one which is called simply "phytase" means 6-phytase. Phytase occurs in higher plants, animals and microorganisms. For example, phytases originated from higher plants such as Mung bean (N.C. Mandal et al., *Phytochemistry*, vol. 11: pp.495-502, (1972)) and wheat (P.E. Lim et al., *Biochemica et Biophysica Acta*, vol. 302: p.316-328, (1973)); phytases originated from microorganisms such as *Pseudomonas* (G.C.J. Irving et al., *Aust. J. Biol. Sci.*, vol. 24: pp.547-557, (1971)), *Bacillus subtilis* (V.K. Paver et al., *J.Bacterial.*, vol. 151: pp.1102-1108, (1982)), *Klebsiella* (Varsha Shah et al., *Indian Journal of Biochemistry and Biophysics*, vol. 27: pp.98-102, (1990)), *Aspergillus* (Abul H.J. Ullah et al., *Preparative Biochemistry*, vol. 17: pp.63-91, (1987)) (European Patent Publication Nos. 0 321 004 and 0 420 358, European patent application No. 92-200414, WO9403612), and *Schwanniomyces castelli* CBS 2863 (P. Galzy et al., *J. Ferment. Bioeng.*, vol. 74.1: pp.7-11, (1992)) are known. It should be noted that *Schwanniomyces castelli* CBS 2863 is now classified into *Schwanniomyces occidentalis* IFO 1840 (Kregerm van Rij et al.: the yeast, a taxonomic study, 3rd ed., Elsevier Sci. Publisher, Amsterdam, The Netherlands, (1984)) (LIST OF CULTURE MICROORGANISMS, 9th ed.: Institute for Fermentation Osaka, pp75-76, (1992)).

Phytic acid (inositol hexaphosphate) which is the substrate of phytase is hexaphosphate of *myo*-inositol (hereinafter also referred to as simply "inositol"). Phytin which is calcium-magnesium mixed salt of phytic acid is contained in all kinds of nuts, cereals, beans, seeds, spores and pollens in an amount of 1-3% as a major reserve substance of phosphate (E. Graf et al., *J. Am. Oil. Chem. Soc.*, vol. 60: pp.1861-1867, (1983)).

Pollution of rivers and the like by the phosphate in excrements of cattle (animals having one stomach) which are bred using feed containing large amount of cereals and seeds is now problematic. As a countermeasure therefor, it is now tried to reduce the concentration of phosphate source in excrements by blending phytase in the feed as a feed additive, thereby decomposing phytate in the feed by the phytase.

However, known phytases lose their activities by 40% after treatment at 68°C for 10 minutes (Abul H.J. Ullah et al., *Preparative Biochemistry*, vol. 18: pp.483-489, (1988)). Therefore, most activity of phytase is lost under the temperature (75-85°C) at which the feed is molded. Thus, feed cannot be molded or drying step of the feed should be largely changed.

On the other hand, it is tried to produce *myo*-inositol by using phytase. *Myo*-inositol is conventionally produced by extracting phytin from corn steep liquor or rice bran and hydrolyzing the extracted phytin at high temperature under high pressure. However, hydrolysis of phytin requires special equipment and large energy, so that its production cost is high.

To overcome this problem, it was proposed to produce inositol by using an enzyme which can hydrolyze phytate at normal temperature under normal pressure. Hydrolysis of phytin by using a microorganism belonging to genus *Aspergillus* (Abul H.J. Ullah et al., *Preparative Biochemistry*, vol. 18: pp.483-489, (1988)) or *Schwanniomyces occidentalis* (*supra*) has been reported.

However, among the enzymes catalyzing hydrolysis of phytin, the phytase produced by a microorganism belonging to genus *Aspergillus* can hydrolyze phytic acid or salts thereof into inositol monophosphate, but further hydrolysis, that is, hydrolysis into *myo*-inositol cannot be attained by this enzyme. Therefore, to carry out the hydrolysis into *myo*-inositol, it is necessary to employ another enzyme such as acid phosphatase together with the phytase. This is not preferred in view of economy.

Recently, it was discovered that *Schwanniomyces occidentalis* produces a phytase which can completely decompose sodium phytate to *myo*-inositol, of which thermal stability is relatively high, 74°C.

In general, since phytase is a kind of phosphatases, its production is induced by culturing a microorganism in a medium having a low concentration of phosphate in order to release the negative control of the production of the enzyme, or by culturing the microorganism in a medium containing a phytate as a sole phosphate source in order to promote the positive control of the production. P. Galzy et al. (*supra*) continuously cultured *Schwanniomyces occidentalis* employing a chemostat in order to keep the concentration of phosphate in the culture medium low. However, the amount of the secreted phytase is as low as 0.15 mg/l. To increase production of the enzyme, one of ordinary skill in the art may consider to produce the enzyme by genetic engineering. However, the gene encoding phytase has not been identified. Further, since phytase is a tetramer containing two types of subunits, that is, subunit α (125 kD) and β (70 kD) ($\alpha:\beta =$

1:3) according to P. Galzy et al. (*supra*), in order to produce the enzyme in a large amount by using genetic engineering, it is necessary to express two types of subunits in a single cell. This requires highly sophisticated genetic engineering method because two kinds of genes encoding the two kinds of subunits, respectively, must be regulated. Further, formation of a molecule having a high-order (4-order) structure in a host cell is not preferred.

SUMMARY OF THE INVENTION

Accordingly, an object of the present invention is to provide a novel phytase which can hydrolyze phytic acid or a salt thereof into *myo*-inositol, which has a simple structure so that it can be produced by a genetic engineering process.

Another object of the present invention is to provide a cloned gene encoding the above-mentioned gene according to the present invention, a recombinant vector containing the gene, and a microorganism transformed with the recombinant vector.

Still another object of the present invention is to provide a method for converting phytate into *myo*-inositol using the cells, treated cells or a culture medium containing the cells of the transformed microorganism.

That is, the present invention provides a phytase consisting essentially of a single type of subunits, which can hydrolyze a phytate to *myo*-inositol. The present invention also provides a cloned gene originated from *Schwanniomyces occidentalis*, which encodes a phytase subunit having a molecular size after removing sugar chains of 50 kD \pm 5 kD determined by SDS-polyacrylamide gel electrophoresis. The present invention further provides a recombinant vector containing the gene according to the present invention, which recombinant vector can express said gene in a host cell. The present invention still further provides a microorganism transformed with the recombinant vector according to the present invention. The present invention still further provides a method for converting a phytate into *myo*-inositol comprising contacting the phytate with the phytase according to the present invention.

Since the phytase according to the present invention can hydrolyze phytates into *myo*-inositol, another enzyme such as acid phosphatase is not required to hydrolyze phytates into *myo*-inositol, which is advantageous from the view point of economy. Since the phytase according to the present invention has only one kind of polypeptide in contrast with the known phytase having two kinds of polypeptides, it is easier to produce the enzyme by genetic engineering. The gene encoding the phytase of the present invention was first cloned and sequenced. A recombinant vector containing the gene and a microorganism transformed with the recombinant vector, which produces the phytase according to the present invention in a large amount were first provided by the present invention. Thus, efficient production of *myo*-inositol in a large amount was first attained by the present invention.

Further, the phytase according to a preferred mode of the present invention has high optimum temperature and high heat resistance, so that enzyme reaction at a temperature which cannot hitherto be carried out can be achieved. Since the gene encoding the phytase according to the present invention was first provided, the present invention will contribute to preparation of phytases (second generation enzymes) having characteristics different from those of the phytase according to the present invention (in terms of optimum pH, optimum temperature, heat resistance, stability to solvents, specific activity, affinity to substrate, secretion ability, translation rate, transcription control and the like). Further, the cloned gene according to the present invention may be employed for screening of phytases having the similar characteristics.

BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1 shows change of phytase activity of culture medium of *Schwanniomyces occidentalis* with time;

Fig. 2 shows the relative activity of purified phytase having a molecular size of 50 kD \pm 5 kD originated from *Schwanniomyces occidentalis*;

Fig. 3 shows temperature dependence of the activity of purified phytase having a molecular size of 50 kD \pm 5 kD originated from *Schwanniomyces occidentalis*;

Fig. 4 shows heat resistance of purified phytase having a molecular size of 50 kD \pm 5 kD originated from *Schwanniomyces occidentalis*;

Fig. 5 shows the results of electrophoresis obtained by electrophoresing purified phytase having a molecular size of 50 kD \pm 5 kD originated from *Schwanniomyces occidentalis* on SDS-polyacrylamide gel;

Fig. 6 shows change with time in the concentration of accumulated *myo*-inositol during the reaction employing the purified enzyme;

Fig. 7 shows the results of Western blot analysis of culture supernatant and cell debris of *Schwanniomyces occidentalis*;

Fig. 8 shows plasmid maps of YEp24 and YEpGPH 1; and

Fig. 9 shows the electrophoretic patterns of the culture supernatant of MT-40539 after silver staining or Western blot analysis.

BEST MODE FOR CARRYING OUT THE INVENTION

The phytase according to the present invention can hydrolyze phytates into *myo*-inositol. That is, it can completely hydrolyze the 6 phosphate groups attached to phytic acid.

5 The phytase according to the present invention consists essentially of a single kind of subunits.

An example of the phytase according to the present invention is the phytase originated from *Schwanniomyces occidentalis*. This phytase is a glycoprotein.

The subunit constituting the phytase originated from *Schwanniomyces occidentalis* has a molecular size after removal of sugar chains of 50 kD \pm 5 kD, which is determined by SDS-PAGE. The subunit contains at least the sequence shown in SEQ ID NO. 1 and/or SEQ ID NO. 2.

10 It is thought that the phytase originated from *Schwanniomyces occidentalis* consists essentially of 3 - 5 subunits (the subunits are the same each other), usually 4 subunits.

The phytase originated from *Schwanniomyces occidentalis* has good heat resistance. That is, the phytase has a residual activity of about 90% after treatment at 70°C for 30 minutes and about 50% after treatment at 75°C for 30 minutes. The good heat resistance is advantageous in using the enzyme as a feed additive as the feed can be molded at a high temperature.

Production of the phytase originated from *Schwanniomyces occidentalis* is induced by culturing the yeast in a medium containing calcium salt of a weak acid and a low concentration of phosphate source. The weak acid may preferably be those acid with which the pH of aqueous solution of the calcium salts thereof is not less than 5.0, more preferably not less than 5.5. As the weak acid, carbonic acid is best preferred. The concentration of the calcium salt of the weak acid may usually be 0.01 - 1% by weight, preferably 0.05 - 0.5% by weight. The term "low concentration" of the phosphate source in the medium herein means 1 to 6000 mg/l, preferably 1 to 600 mg/l. By culturing *Schwanniomyces occidentalis* under the inductive conditions described above, the phytate is secreted and accumulated in the culture medium.

The cause of the inductive secretion of the phytase originated from *Schwanniomyces occidentalis* is not clear. However, the present inventors discovered that when the yeast is cultured in a medium containing a phytate as a sole phosphate source, the phytase activity is scarcely detected in the culture medium, while by adding a calcium salt, the phytase activity is prominently increased. Thus, it is thought that the reason why the production of phytase is induced by calcium salt may be that the suppression of phytase gene by the phosphate liberated in a small amount by decomposition of phytin is cancelled by the calcium salt.

30 The gene encoding the subunit of the phytase originated from *Schwanniomyces occidentalis* may be cloned by various methods. However, in view of the fact that yeast is a eukaryote and so the gene may contain introns, it is preferred to clone cDNA prepared from the mRNA of the gene. More particularly, for example, cDNAs prepared from mRNAs of *Schwanniomyces occidentalis* are inserted into an expression vector for *E. coli* to prepare a cDNA library, and the desired clone may be obtained by selecting a clone specifically reacts with an antibody to the subunit as a probe. An example of this process is detailed in the examples described below.

35 The cDNA encoding the subunit of the phytase originated from *Schwanniomyces occidentalis* has a length of 1631 bp, of which sequence is shown in SEQ ID NO. 5. This sequence contains the nucleotide sequences shown in SEQ ID NOs. 3 and 4.

40 It is well-known in the art that there are cases wherein the activity of an enzyme is retained even if the amino acid sequence of an enzyme is modified to a small extent, that is, even if one or more amino acids in the amino acid sequence are substituted or deleted, or even if one or more amino acids are added to the amino acid sequence. In view of the fact that such modifications of the amino acid sequence can be easily carried out by, for example, site-specific mutagenesis, it is intended that the enzymes as well as the cloned genes encoding the enzymes which have the same amino acid sequence shown in SEQ ID NO. 5 except that one or more amino acids in the amino acid sequence are substituted or deleted, or one or more amino acids are added are within the scope of the present invention as long as the resulting enzyme is within the definition of the present invention, that is, the enzyme can hydrolyze a phytate to *myo*-inositol and the enzyme consists essentially of a single type of subunits.

The cloned gene encoding the subunit of the phytase originated from *Schwanniomyces occidentalis* may be expressed in a host other than *Schwanniomyces occidentalis* by inserting the gene into a vector replicable in the host cell to obtain a recombinant vector and transforming the host cell with the recombinant vector. An example of the recombinant vector containing the gene encoding the subunit of the phytase originated from *Schwanniomyces occidentalis* is YEpGHP 1 (Fig. 8) which was prepared in the example described below.

50 The desired clone may also be obtained by partially digesting the genome of *Schwanniomyces occidentalis*, preparing a genome library therefrom, and selecting the clone which hybridizes with the above-mentioned cDNA encoding the subunit of the phytase originated from *Schwanniomyces occidentalis*.

55 By transforming an appropriate host with the recombinant vector containing the gene encoding the subunit of the phytase originated from *Schwanniomyces occidentalis*, the gene can be expressed and the phytase can be produced in the host cells, which may be secreted.

To express the gene encoding the subunit of the phytase originated from *Schwanniomyces occidentalis*, it is preferred to utilize a host-vector system by which an exogenous protein can be produced in a host cell. Thus, it is advantageous to utilize the host-vector system employing as the host *E. coli*, *Bacillus subtilis*, a yeast or a mold fungus. The gene may be expressed by ligating the gene at a downstream site of a promoter and preferably a secretion signal which are known to be effective in the host cell, inserting the resultant into an expression vector replicable in the host cell, and transforming the host cell with the recombinant vector. Alternatively, the gene ligated to the promoter and the secretion signal may be inserted into the chromosome of the host cell. It should be noted that the gene may be inserted into an expression vector which preliminarily has the above-mentioned promoter and the secretion signal.

The present inventors succeeded in producing the phytase originated from *Schwanniomyces occidentalis* by inserting the genome DNA fragment from this yeast into a vector plasmid YEp24 for *Saccharomyces cerevisiae* and transforming *Saccharomyces cerevisiae* with the prepared recombinant plasmid.

As described in the examples below, the present inventors succeeded in preparing transformants which secrete the phytase originated from *Schwanniomyces occidentalis* by the method described above, which transformants are *Escherichia coli* MT-10743 and *Saccharomyces cerevisiae* MT-40539. These transformants have been deposited under the Budapest Treaty, the details of the depositions being described in the examples below.

The transformants may be cultured by an ordinary culturing method for the microorganism.

Although the culture medium for the transformants is not restricted and any culture media may be employed which are suited for the microorganism, it is preferred to add calcium salt of the above-mentioned weak acid to cancel the suppression of expression of phytase by the liberated phosphate. The preferred concentration of the calcium salt is the same as described above.

The phytase according to the present invention may be produced by culturing the transformants under normal conditions. To use the phytase for various uses, the culture medium, cells and treated cells may be used as the source of the phytase. The treated cells include cell debris obtained by disrupting the cells by self digestion, by lysisation by an organic solvent, by ultrasonic disruption or by homogenization; the above-mentioned cell debris which was partially purified; phytase protein separated from the culture medium or the cells; and the materials in which the cells obtained by culturing or the phytase protein separated from the cells or the culture medium are immobilized in a carrier such as sodium alginate, κ -carrageenan or polyacrylamide.

The phytase according to the present invention may be employed as an enzyme source for various uses, such as, for example, feed additive and production of inositol.

A phytate may be converted into myo-inositol by adding the above-mentioned phytase source to a buffer solution containing a phytate such as calcium phytate, and carrying out the reaction. The reaction may be carried out, for example, at 5 to 90°C for 1 hour to 1 week. The concentrations of the phytate and the phytase may be, for example, 0.02 mg/l to 200 g/l and 0.1 mg/l to 10 g/l, respectively.

35 Examples

The present invention will now be described in more detail by way of examples. It should be noted that the examples are presented for the illustration purpose only and should not be interpreted in any restrictive way.

40 Example 1 Induction of High Expression of Phytase Gene by Addition of Calcium Carbonate

A medium containing, per one liter, 10 g of glucose, 3 g of $(\text{NH}_4)_2\text{SO}_4$, 0.5 g of MgSO_4 , 0.5 g of KCl, 0.1 g of CaCl_2 , 0.135 g of FeCl_3 , minor metals, vitamins other than inositol, 0.03 g of yeast extract for initial growth, 0.6 g of calcium phytate as a sole phosphate source, and 1 g of CaCO_3 for induction of high expression of phytase gene, was prepared. Thirty milliliters of this medium was placed in an Erlenmeyer flask equipped with a baffle and *Schwanniomyces occidentalis* IFO 1840 was inoculated to the medium, followed by culturing the medium at 28°C for 2 days. As a control, the same procedure as mentioned above was carried out except that the medium did not contain CaCO_3 .

After the culture, the culture medium was 10-fold concentrated by ultrafiltration using Amicon Centricron 30 micro-concentrator, followed by dialysis against deionized water at 4°C for 2 hours 4 times. The phytase activity of the dialyzed liquid was measured as follows. That is, 900 μl of an aqueous solution of the substrate (60 mM sodium acetate buffer (pH 4.4) containing 5 mM sodium phytate) was added to 100 μl of the dialyzed liquid and reaction was allowed to occur at 70°C for 30 minutes. The reaction was stopped by adding 100 μl of 5N H_2SO_4 in the reaction mixture. As a control, the same procedure was carried out except that 100 μl of 5N H_2SO_4 was added to the substrate solution before the reaction. After stopping the reaction, the reaction mixture was diluted in a serial fashion from 1 to 2048-fold in wells of a 96-well microtiter plate. Phosphate-detecting solution (solution A: 1.47 g/l of Malachite Green, 20% H_2SO_4 ; solution B: 7.5% ammonium molybdate; solution C: 11% (w/v) of Tween 20; the solutions A, B and C were mixed at a ratio of 50:12.5:1 immediately before use) was added in an amount of 50 μl per 100 μl of the diluted solution, and the mixture was shaken for 30 minutes, followed by measurement of absorbance at 620 nm. Based on a calibration curve in a range of 1 - 10 nM of phosphate, the amount of released phosphate was calculated from the measured value. One unit of

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phytase activity was defined as the activity by which 1 μ mol of phosphate is released per minute. The results are shown in Fig. 1. In Fig. 1, symbol "○" shows the results wherein CaCO_3 was added and symbol "●" shows the results wherein CaCO_3 was not added. As is apparent from Fig. 1, phytase activity was detected in the culture medium to which calcium carbonate was added while almost no phytase activity was detected in the culture medium to which calcium carbonate was not added.

Example 2 Measurement of Phytase Activity and Molecular Size

(1) Removal of Sugar Chains of Enzyme

Purification of the enzyme which was induced under the conditions described above and secreted and accumulated in the medium in Example 1 was tried in order to identify the enzymatic properties of the phytase.

It was confirmed that the enzyme is a glycoprotein by a preliminary experiment, that is, by SDS-PAGE. It is likely that a glycoprotein does not give a clear band in electrophoresis. Thus, in order to obtain a single band in electrophoresis, sugar chains were preliminarily removed by Endoglycosidase H (Endo H, commercially available from Boehringer Mannheim Biochemica). That is, the enzyme was denatured by treatment in a solution containing 10 mM of sodium acetate (pH 5.2), 100 mM of 2-mercaptoethanol and 0.0025% of SDS, the mentioned concentrations being final concentrations, at 95°C for 5 minutes, and the resultant was slowly allowed to cool to room temperature. Then Endo H was added in an amount of 4 μ U per 1 ng of protein and reaction was allowed to occur at 37°C overnight.

It should be noted that, in the experiments described below, the samples of which enzyme activities are measured or which are subjected to electrophoresis were treated in a solution containing 10 mM sodium acetate (pH 5.2) to which Endo H is added in an amount of 4 μ U per 1 ng of protein at 37°C overnight.

(2) Detection of Hydrolyzing Activity of Crude Enzyme and Measurement of Molecular Size

The crude enzyme obtained by removing sugar chains by Endo H in Example 2(1) was subjected to Native PAGE. By silver staining and hydrolytic activity staining, a single band which exhibited hydrolytic activity was detected.

The hydrolytic activity staining was carried out by incubating overnight the gel after electrophoresis in a solution containing 0.1% α -naphthylphosphate, 0.2% first garnet GBC salt and 0.6 M sodium acetate buffer (pH 5.0). By this staining, a band having hydrolytic activity is stained in black. To confirm the phytase activity of the polypeptide corresponding to the band stained in black, the polypeptide corresponding to the band was reacted with sodium phytate, and generated phosphate and *myo*-inositol were quantified. As a result, generation of phosphate and *myo*-inositol was observed.

The molecular size of this polypeptide was measured by SDS-PAGE. The results are shown in Fig. 5. In Fig. 5, lane 1 shows the electrophoretic pattern of molecular size Marker H (commercially available from BIORAD); lane 2 shows the pattern of molecular size Marker L (commercially available from BIORAD); lane 3 shows the pattern of purified enzyme before removal of sugar chains; lane 4 shows the pattern of purified enzyme after removal of sugar chains by the method described in Example 2; lane 5 shows the pattern of purified enzyme after removal of sugar chains by using 20 units of Endo H; lane 6 shows the pattern of purified enzyme after removal of sugar chains by using 20 units of Endo H without the denaturing treatment before the reaction with Endo H; and lane 7 shows the pattern of Endo H alone. As can be seen from Fig. 5, the molecular size of the purified subunit is 50 kD \pm 5 kD. Thus, this polypeptide is apparently different from the known α and β subunits of *Schwanniomyces occidentalis*.

To analyze the enzyme in more detail, the polypeptide was purified (see below) and antibody against the purified polypeptide was prepared by immunizing a rabbit with the polypeptide and purifying the antibody by applying the antiserum from the rabbit to affinity chromatography (see below). Western blot analysis using this antibody revealed that this antibody reacted with a band corresponding to a molecular size of 50 kD. As mentioned above, the molecular sizes of α and β subunits of the known phytase of *Schwanniomyces occidentalis* are 125 kD and 70 kD, respectively. In view of the large differences in molecular sizes, it is concluded that the enzyme having phytase activity, which is produced by culturing *Schwanniomyces occidentalis* in a medium containing calcium carbonate, is a novel enzyme which is different from the known phytase containing α and β subunits.

Example 3 Purification of Phytase from Culture Supernatant

Schwanniomyces occidentalis was inoculated to 20 ml of the medium described in Example 1, and the medium was incubated overnight at 28°C. The whole culture medium was then aseptically added to 2 liters of the same medium and the obtained culture medium was incubated at 28°C for 2 days. The resultant was centrifuged to obtain about 2 liters of culture supernatant. The obtained culture supernatant was concentrated to 200 ml at 50-60°C by an evaporator and the obtained concentrate was dialyzed against 20 mM Tris-HCl buffer at 4°C for 2 hours 4 times. The resulting dialyzate was concentrated to 20 ml by the evaporator and the obtained concentrate was dialyzed against 20 mM Tris-HCl buffer at

4°C for 2 hours 4 times. The obtained crude enzyme solution was applied to 10 ml of Q-Sepharose fast flow column (commercially available from Pharmacia) and then the column was washed with 50 ml of 20 mM Tris-HCl buffer, pH 7.5. Elution was performed by passing 20 ml each of 20 mM Tris-HCl buffer containing NaCl at a concentration of 25, 50, 75, 100, 125, 150, 175 or 200 mM in the order mentioned. Fractions were collected every 20 ml and phytase activity of each fraction was measured after dialysis against deionized water at 4°C for 2 hours 4 times.

The optimum pH, optimum temperature and heat resistance of the obtained enzyme were determined.

The optimum pH of the enzyme was measured by measuring the activity of the enzyme by the method described in Example 1, wherein pH during the measurement of enzyme activity was changed using 20 mM sodium acetate buffer or 20 mM phthalate buffer.

The results are shown in Fig. 2. In Fig. 2, the relative activity is defined taking the activity of the enzyme when the enzyme reaction is carried out in 20 mM sodium acetate buffer (pH 4.4) as 100%. In Fig. 2, the symbol "○" shows the results wherein 20 mM sodium acetate buffer was used and the symbol "●" shows the results wherein 20 mM phthalate buffer was used. As can be seen from Fig. 2, the optimum pH of this enzyme is between 2.7 and 5.0.

The optimum temperature of the enzyme was measured by measuring the activity of the enzyme by the method described in Example 1, wherein the temperature during the enzyme reaction was changed. The results are shown in Fig. 3. In Fig. 3, the relative activity is defined taking the activity of the enzyme when the enzyme reaction is carried out at 70°C. As shown in Fig. 3, the optimum temperature of this enzyme is about 70°C.

The heat resistance of the enzyme was determined by incubating the enzyme in 20 mM sodium acetate buffer (pH 4.4) for 30 minutes at varying temperature and the enzyme activity of the heat treated solution was measured by the method described in Example 1. The results are shown in Fig. 4. In Fig. 4, the relative activity is defined taking the activity of the enzyme before the incubation. As can be seen from Fig. 4, the residual activity of the enzyme was about 90% at 70°C and about 50% at 75°C.

Example 4 Production of *myo*-inositol by Phytase

To a solution (pH 4.0) containing 100 g/l of calcium phytate, the purified phytase obtained in Example 3 was added to a concentration of 8 U/ml, and the mixture was allowed to react at 50°C. The accumulated *myo*-inositol was quantified by high performance liquid chromatography. The results are shown in Fig. 6.

Example 5 Determination of Amino Acid Sequence of N-terminal Region

The purified enzyme was treated with Endo H to remove sugar chains and the resultant was applied to Bio-Rad Prep-Cell Model 491 to eliminate those molecules in which removal of sugar chains was incomplete. The resulting enzyme was electrophoresed by 12.5% SDS-PAGE, and the pattern was electrophoretically transferred to a PVDF blotting membrane filter (IMMUNOVIRON, commercially available from Millipore) by a Sartorius blotting apparatus. After washing the membrane filter, the positions of proteins were determined based on coloring by Ponceau reagent. The band of interest was cut out and dried, and the sequence of the N-terminal region of the enzyme was determined by an amino acid sequencer (commercially available from Shimadzu Corp). The determined sequence is shown in SEQ ID NO. 1 in Sequence Listing.

Example 6 Determination of Amino Acid Sequence of N-terminal Region of Partial Digest by V8 Protease

The enzyme exhibiting a molecular size of 50 kD from which sugar chains were removed by the method described in Example 2 was dissolved in a sample buffer (125 mM Tris-HCl (pH 6.8) containing 0.1% SDS and 10% glycerol) in an amount of 200 - 400 µg. On the other hand, 1 µg of V8(Glu-c) protease originated from a microorganism belonging to genus *Staphylococcus* was dissolved in buffer for protease (125 mM Tris-HCl (pH 6.8) containing 0.1% SDS and 5% glycerol).

On 17% SDS-PAGE gel, the phytase solution was mounted and then the V8 protease solution was slowly overlaid. The resultant was electrophoresed. When the BPB marker reached the vicinity of the border between the stacking gel and the separation gel, the electrophoresis was stopped for 30 minutes, thereby allowing reaction between the protease and the phytase. Then electrophoresis was restarted and the sequence of the N-terminal region of the fragment resulting from the partial digestion of the phytase was determined by the method described in Example 4. The determined sequence is shown in SEQ ID NO. 2 in Sequence Listing.

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Example 7 Screening of Phytase cDNA

(1) Preparation of Antibody

5 One hundred microliters of a solution (1 mg/ml) of the enzyme exhibiting a molecular size of 50 kD from which sugar chains were removed by the method described in Example 2(1) was mixed with 100 µl of Freund's complete adjuvant (commercially available from DIFCO) and the mixture was emulsified. The obtained emulsion was used as an immunogen.

10 The immunogen was subcutaneously administered to a rabbit in several times and booster was administered at 2, 4 and 6 weeks after the first immunization. The increase of the antibody titer was monitored by ELISA comparing the measured titer with the titer measured before the immunization.

After the above-described immunization, serum was recovered and the antibody was purified by affinity column prepared by coupling 1 mg of the purified phytase after the removal of sugar chains to 0.1 g of CNBr-activated Sepharose 4B (commercially available from Pharmacia).

15 Using the thus purified antibody, Western blot analysis was performed on the crude enzyme after removing sugar chains. The results are shown in Fig. 7. In Fig. 7, lane 1 shows the electrophoretic pattern of molecular size Marker L (commercially available from BIORAD); lanes 2 and 3 show the SDS-PAGE patterns of the culture supernatant and cell debris, respectively; and lanes 4 and 5 show the results of Western blot analysis of the culture supernatant and cell debris, respectively, which were electrophoresed under the same conditions in the SDS-PAGE as those of lanes 2 and 3. As can be seen from Fig. 7, a band corresponding to a molecular size of 50 kD which is thought to be the band of the enzyme, and a band corresponding to a molecular size of 30 kD which is thought to be a fragment generated by decomposition of the enzyme were stained by the antibody.

(2) Cloning of Phytase cDNA

25 *Schwanniomyces occidentalis* was cultured by the method described in Example 4 until absorbance at 660 nm reached 1.0. After collecting the cells by centrifugation, the cells were washed with sodium acetate buffer (pH 3.5) to remove precipitated CaCO₃ and then with 10 mM Tris-HCl pH 7.0.

30 The obtained cells were disrupted by freezing the cells by liquid nitrogen and grinding the frozen cells in a mortar together with sea sand. To the obtained powder, the extraction buffer of Quick Prep mRNA purification kit (commercially available from Pharmacia) was added and the resultant was uniformly mixed, followed by centrifugation at 4°C at 2000 g. The supernatant was collected, thereby collecting the total RNAs. In accordance with the instructions of Quick Prep mRNA purification kit, mRNAs were recovered. Then cDNAs were synthesized using a commercially available kit (Uni-ZAP cDNA Library kit (commercially available from STRATAGENE) and the obtained cDNAs were packaged using a commercially available kit (GIGAPACK GOLD II, STRATAGENE), thereby preparing a cDNA library.

35 The cDNAs were expressed by IPTG induction and the obtained 50,000 plaques were transferred to a PVDF blotting membrane filter (IMMUNOVIRON, commercially available from Millipore) in accordance with the instructions of UniZAP cDNA Library kit (commercially available from STRATAGENE), followed by screening with the antibody prepared above as a probe. The cDNA of the clone reacted with the antibody was subcloned into pBluescript SK- by in vivo excision. 40 The obtained recombinant *Escherichia coli* MT-10743 was deposited in National Institute of Bioscience and Human-Technology, Agency of Industrial Science and Technology at 1-3, Higashi 1-chome, Tsukuba-shi, Ibaraki-ken, 305 Japan on April 21, 1994 under accession No. FERM P-14287 and the deposition was converted to international deposition under the Budapest Treaty on May 25, 1995, under accession No. FERM BP-5108. The subcloned cDNA was sequenced and the determined nucleotide sequence was the same as that shown in SEQ ID NO. 5. In this nucleotide sequence, 45 the nucleotide sequences shown in SEQ ID NOs. 3 and 4 are contained at 11-34 nt and 377-400 nt, respectively.

Example 8 Cloning of Phytase Genome DNA

50 One platinum loop of *Schwanniomyces occidentalis* was inoculated to 5 ml of YEPD medium (containing 10% yeast extract, 20% polypeptone, 20% glucose) and the culture medium was incubated overnight at 30°C. The culture medium was then aseptically inoculated to 1 liter of YEPD medium. Culture was continued until the absorbance at 660 nm reached 5.0 and the culture medium was centrifuged at 2000 x g to recover the cells. The obtained cells were suspended in 30 ml of lysis buffer (1M sorbitol, 25 mM EDTA, 50 mM MES (pH 5.5), 4 mg/ml of Novozyme 234 (commercially available from Novo Biolabs), 20 mg/ml of Zymolyase (commercially available from Seikagaku)) and the suspension was incubated 55 at 30°C for 1 hour. After confirming that the cells were converted to protoplasts, 500 µl of diethyl pyrocarbonate, 1.2 ml of 0.5M EDTA, 1.6 ml of 0.2M Tris base and 1.6 ml of 10% SDS were added and the resultant was well mixed, followed by incubation at 4°C for 30 minutes.

Thereafter, 3.5 ml of 5M potassium acetate was added and the suspension was centrifuged at 2000 g for 10 minutes, followed by recovery of supernatant. The obtained supernatant was treated with equivolume of phenol/chloroform three

times and then equivolume of 2-propanol was added, followed by incubation at -20°C for 2 hours. After centrifugation at 3000 g for 10 minutes, the precipitate was washed twice with 70% ethanol and dried. The dried precipitate was dissolved in 2 ml of TE buffer and 1/100 volume of 1 mg/ml RNase was added to the solution, followed by incubation of the resulting mixture at 37°C for 30 minutes.

5 The resulting solution was treated twice with equivolume of phenol/chloroform and 1/10 volume of 3M sodium acetate was added. To the resultant, twice volume of ethanol was added and the mixture was left to stand at -20°C for 2 hours.

The obtained DNA was partially digested with a restriction enzyme *Sau3AI*, and a genome library was prepared from 9-23 kb fragments using a commercially available kit (LAMBDA EMBL 3/*Bam*HI VECTOR KIT (commercially available from STRATAGENE)).

10 Using the thus prepared genome library, the fragment containing the gene encoding the phytase of interest was cloned in accordance with the instructions of LAMBDA EMBL 3/*Bam*HI VECTOR KIT, STRATAGENE. In this procedure, the cDNA obtained in Example 7 was used as the probe.

Among the obtained fragments, *Xho*I fragment of about 5.3 kb was subcloned into a vector plasmid YEp24 at *Sal*I site to obtain a recombinant vector YEpGPH 1 (Fig. 8). The plasmid YEp24 was extracted from ATCC-37051 by a conventional method.

Example 9 Breeding of Yeast Secreting Phytase Originated from *Schwanniomyces occidentalis*

In accordance with the method of Ito et al. (Ito, H., Y. Jukuda, K. Murata and A. Kimura, J. Bacteriol., Vol. 153, pp.163-168, (1983)), *Saccharomyces cerevisiae* W303-1B (Mat α ade2-1 his3-11,15 leu2-3,112 ura3-1 trp1-1 can1-100) was transformed with the recombinant plasmid (YEpGPH 1) obtained in Example 8. As a result, a transformant MT-40539 was obtained, which was deposited in the above-mentioned National Institute of Bioscience and Human Technology on May 25, 1994 under accession No. FERM P-14333 and the deposition was converted to international deposition under the Budapest Treaty on May 25, 1995, under accession No. FERM BP-5109.

25 The transformant MT-40539 and *Saccharomyces cerevisiae* W303-1B transformed with the vector plasmid YEp24 as a control were cultured in a medium described in Example 1 to which required nutrients (20 mg/l of adenine, 20 mg/l of histidine, 30 mg/l of leucine, 20 mg/l of tryptophan) had been added and the phytase activities of the cultured cells were measured. As a result, MT-40539 exhibited higher phytase activity than that exhibited by *Saccharomyces cerevisiae* W303-1B transformed with the vector plasmid YEp24. The culture supernatant was subjected to Western blot analysis using the antibody obtained in Example 7(1). As a result, a protein recognized by the antibody was detected. The pattern of the Western blot analysis is shown in Fig. 9. In Fig. 9, lanes 1 and 6 show electrophoretic patterns of molecular size Marker L (commercially available from BIORAD); lanes 2 and 7 show the patterns of phytase purified from culture supernatant of *Schwanniomyces occidentalis*; lanes 3 and 8 are vacant lanes; lanes 4 and 9 show the patterns of the samples obtained by removing sugar chains of the phytase by Endo H, which was obtained from the culture supernatant of the transformants prepared by transforming *Saccharomyces cerevisiae* W303-1B with YEp24; and lanes 5 and 10 show the patterns of the samples obtained by removing sugar chains of the phytase by Endo H, which was obtained from the

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culture supernatant of MT-40539.

SEQUENCE LISTING

5 SEQ ID NO.: 1

SEQUENCE LENGTH: 8

SEQUENCE TYPE: amino acid

10 TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGMENT TYPE: internal fragment

15 ORIGINAL SOURCE:

ORGANISM: *Schwaniomyces occidentalis*

20 INDIVIDUAL ISOLATE: wild type

FEATURE: N-terminal

SEQUENCE DESCRIPTION

25 Val Ser Ile Ser Lys Leu Ile Asn

1 5

SEQ ID NO.: 2

30 SEQUENCE LENGTH: 8

SEQUENCE TYPE: amino acid

TOPOLOGY: linear

35 MOLECULE TYPE: peptide

FRAGMENT TYPE: internal fragment

ORIGINAL SOURCE:

40 ORGANISM: *Schwaniomyces occidentalis*

INDIVIDUAL ISOLATE: wild type

45 FEATURE: N-terminal of fragment obtained by partial digestion with
V8 protease

SEQUENCE DESCRIPTION

50 Thr Ser Ala Leu Asn Ser Gln Gly

55

1 5

5 SEQ ID NO.: 3
SEQUENCE LENGTH: 24
SEQUENCE TYPE: nucleic acid
10 STRANDEDNESS: double
TOPOLOGY: linear
15 MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: *Schwaniomyces occidentalis*
20 INDIVIDUAL ISOLATE: wild type
SEQUENCE DESCRIPTION
25 GTCTCGATCT CAAAATTAAT TAAT 24
SEQ ID NO.: 4
SEQUENCE LENGTH: 24
30 SEQUENCE TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
35 MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
40 ORGANISM: *Schwaniomyces occidentalis*
INDIVIDUAL ISOLATE: wild type
SEQUENCE DESCRIPTION
45 ACAAGTGCAC TGAAGTCGCA AGGT 24
SEQ ID NO.: 5
50 SEQUENCE LENGTH: 1631
SEQUENCE TYPE: nucleic acid
STRANDEDNESS: double
55

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TOPOLOGY: linear

5 MOLECULE TYPE: cDNA

ORIGINAL SOURCE:

10 ORGANISM: *Schwaniomyces occidentalis*

INDIVIDUAL ISOLATE: wild type

SEQUENCE DESCRIPTION

15	GTCAATC ATG GTC TCG ATC TCA AAA TTA ATT AAT AAC GGT TTA CTC TTA	49
	Met Val Ser Ile Ser Lys Leu Ile Asn Asn Gly Leu Leu Leu	
	1 5 10	
20	GCT GGT CAA AGT GTT TAC CAA GAT TTA GCT ACT CCA CAA CAA TCT TCC	97
	Ala Gly Gln Ser Val Tyr Gln Asp Leu Ala Thr Pro Gln Gln Ser Ser	
	15 20 25 30	
25	GTC GAG CAG TAT AAT ATT ATT AGG TTT TTA GGT GGT TCG GGT CCT TAC	145
	Val Glu Gln Tyr Asn Ile Ile Arg Phe Leu Gly Gly Ser Gly Pro Tyr	
	35 40 45	
30	ATT CAA CGC AGT GGT TAT GGT ATT TCC ACT GAT ATT CCT GAT CAG TGC	193
	Ile Gln Arg Ser Gly Tyr Gly Ile Ser Thr Asp Ile Pro Asp Gln Cys	
	50 55 60	
35	ACA ATT AAG CAA GTT CAG TTG ATG TCA AGG CAT GGG GAA AGA TAC CCT	241
	Thr Ile Lys Gln Val Gln Leu Met Ser Arg His Gly Glu Arg Tyr Pro	
40	65 70 75	
	TCA AAA AAC TCT GGT AAG AAG TTA AAA ACA ATA TAT GGT AAA TTA AAG	289
	Ser Lys Asn Ser Gly Lys Lys Leu Lys Thr Ile Tyr Gly Lys Leu Lys	
45	80 85 90	
	AGC TAC AAT GGC ACT TTC ACA GGT AGC TTA GCT TTT TTG AAT GAC TAT	337
50	Ser Tyr Asn Gly Thr Phe Thr Gly Ser Leu Ala Phe Leu Asn Asp Tyr	
	95 100 105 110	

55

	GAA TAT TTT GTT CCG GAT GAT AGT TTG TAC GAA AAG GAA ACA AGT GCA	385
5	Glu Tyr Phe Val Pro Asp Asp Ser Leu Tyr Glu Lys Glu Thr Ser Ala	
	115 120 125	
	CTG AAC TCG CAA GGT TTA TTT GCA GGT ACT ACA GAT GCC TTA AGA CAT	433
10	Leu Asn Ser Gln Gly Leu Phe Ala Gly Thr Thr Asp Ala Leu Arg His	
	130 135 140	
	GGT GCT GCT TTT AGA GCT AAA TAT GGA TCA TTG TAT AAA CAA AAT TCT	481
15	Gly Ala Ala Phe Arg Ala Lys Tyr Gly Ser Leu Tyr Lys Gln Asn Ser	
	145 150 155	
	ACC TTG CCA GTT TTC ACT TCA AAT TCC AAC AGA GTC TAC CAG ACT TCT	529
20	Thr Leu Pro Val Phe Thr Ser Asn Ser Asn Arg Val Tyr Gln Thr Ser	
	160 165 170	
	GAA TAC TTT GCC AGA GGT TTC TTA GGT GAT GAA TTT TCT GAT GCT ACT	577
25	Glu Tyr Phe Ala Arg Gly Phe Leu Gly Asp Glu Phe Ser Asp Ala Thr	
	175 180 185 190	
	GTT CAC TTT GCT ATC ATT GAT GAA GAC CCT AAA ATG GGT GTT AAT TCA	625
30	Val His Phe Ala Ile Ile Asp Glu Asp Pro Lys Met Gly Val Asn Ser	
	195 200 205	
	TTA ACA CCA AGA GCC GCT TGT GAC AAT TAT AAT GAG GAT GTG AAT GAC	673
35	Leu Thr Pro Arg Ala Ala Cys Asp Asn Tyr Asn Glu Asp Val Asn Asp	
	210 215 220	
	GGC ATT GTC AAT CAA TAT AGC ACT GAC TAT TTG GAT GAA GCC CTT AAA	721
40	Gly Ile Val Asn Gln Tyr Ser Thr Asp Tyr Leu Asp Glu Ala Leu Lys	
	225 230 235	
	AGA TTC CAA TCA TCA AAT CCA GGA TTG AAT TTG ACC TCG GAA GAC GTT	769
45	Arg Phe Gln Ser Ser Asn Pro Gly Leu Asn Leu Thr Ser Glu Asp Val	
50	240 245 250	
55		

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5	TAC CAA CTT TTC GCT TAC TGT GCA TAT GAG ACT AAT GTT AAG GGT GCA	817
	Tyr Gln Leu Phe Ala Tyr Cys Ala Tyr Glu Thr Asn Val Lys Gly Ala	
	255 260 265 270	
10	TCC CCA TTC TGT GAC TTA TTT ACT AAT GAA GAA TAC ATT CAA TAT TCC	865
	Ser Pro Phe Cys Asp Leu Phe Thr Asn Glu Glu Tyr Ile Gln Tyr Ser	
	275 280 285	
15	TAC AGC GTT GAT CTT TCT AAT TAT TAT TCT CAC GGG GCA GGT CAT AAT	913
	Tyr Ser Val Asp Leu Ser Asn Tyr Tyr Ser His Gly Ala Gly His Asn	
	290 295 300	
20	CTA ACT AAA ACC ATT GGT TCT ACT TTA TTA AAT GCC TCA TTA ACC TTA	961
	Leu Thr Lys Thr Ile Gly Ser Thr Leu Leu Asn Ala Ser Leu Thr Leu	
	305 310 315	
25	TTA AAA GAT GGC ACC AAT GAC AAT AAA ATC TGG TTA TCT TTT TCA CAC	1009
	Leu Lys Asp Gly Thr Asn Asp Asn Lys Ile Trp Leu Ser Phe Ser His	
	320 325 330	
30	GAT ACT GAT TTG GAA ATC TTC CAT AGT GCC TTA GGA ATT GTT GAG CCA	1057
	Asp Thr Asp Leu Glu Ile Phe His Ser Ala Leu Gly Ile Val Glu Pro	
	335 340 345 350	
35	GCT GAA GAT TTA CCA GTT GAT TAC ATT CCT TTT CCA TCG CCA TAT ATT	1105
	Ala Glu Asp Leu Pro Val Asp Tyr Ile Pro Phe Pro Ser Pro Tyr Ile	
40	355 360 365	
	CAC TCA CAA ATT GTT CCA CAA GGT GCT AGA ATT TAT ACT GAG AAA TAT	1153
	His Ser Gln Ile Val Pro Gln Gly Ala Arg Ile Tyr Thr Glu Lys Tyr	
45	370 375 380	
	TCA TGT GGC AAC GAA ACC TAT GTT AGA TAT ATA CTT AAT GAT GCA GTT	1201
50	Ser Cys Gly Asn Glu Thr Tyr Val Arg Tyr Ile Leu Asn Asp Ala Val	
	385 390 395	

55

GTT CCA ATT CCA AAA TGC TCT TCT GGT CCA GGG TTC TCA TGT GAG CTT 1249
 5 Val Pro Ile Pro Lys Cys Ser Ser Gly Pro Gly Phe Ser Cys Glu Leu
 400 405 410
 AGT AAA TTC GAA GAA TAT ATT AAT AAA AGA CTT AGG GAT GTT GAC TTT 1297
 10 Ser Lys Phe Glu Glu Tyr Ile Asn Lys Arg Leu Arg Asp Val Asp Phe
 415 420 425 430
 GTT GAA CAA TGT GAT TTA AAA GAT GCT CCA ACT GAA GTT ACT TTT TAC 1345
 15 Val Glu Gln Cys Asp Leu Lys Asp Ala Pro Thr Glu Val Thr Phe Tyr
 435 440 445
 TGG GAT TAC ACG TCG GTG AAC TAT AGT GCG TCC CTT ATT AAT GGT 1390
 20 Trp Asp Tyr Thr Ser Val Asn Tyr Ser Ala Ser Leu Ile Asn Gly
 450 455 460
 TAAATTGAGT ATAGGAGAAT ATCTTATTTT TAGTTTGATC ACTATCTGAA TCCACTTTGC 1450
 TCTTTCTCCT TGTTTGTATT GCTTATCCAT TGTTTAGAAA TACGTTATAA AGCAATCATT 1510
 TTTACAATA TGTCGTCTAA TACTTTGTTT CTAGAATTAA AAAAATAAAT AGTATACCTG 1570
 30 TGTAAGTCT TACTTGATAG CTAAGTAGTC ACTTCTTAAT CATACACCTA ATCTATCCTA 1630
 A 1631
 35
 40
 45
 50
 55

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SEQUENCE LISTING

5

(1) GENERAL INFORMATION:

(i) APPLICANT:

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(I) TELEX: 2223622MTCHEM J

10

15

(ii) TITLE OF INVENTION: Novel Phytase

(iii) NUMBER OF SEQUENCES: 6

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

20

(v) CURRENT APPLICATION DATA:

APPLICATION NUMBER: EP 95110503.0

25

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

35

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Schwaniomyces occidentalis
(B) STRAIN: wild type

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Val Ser Ile Ser Lys Leu Ile Asn
1 5

45

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: peptide

55

(v) FRAGMENT TYPE: internal

5 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Schwaniomyces occidentalis
(B) STRAIN: wild type

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
Thr Ser Ala Leu Asn Ser Gln Gly
1 5

15 (2) INFORMATION FOR SEQ ID NO: 3:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: cDNA
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Schwaniomyces occidentalis
(B) STRAIN: wild type

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
GTCTCGATCT CAAAATTAAT TAAT 24

30 (2) INFORMATION FOR SEQ ID NO: 4:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Schaniomyces occidentalis
40 (B) STRAIN: wild type

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
45 ACAAGTGCAC TGAATCGCA AGGT 24

(2) INFORMATION FOR SEQ ID NO: 5:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1631 base pairs
50 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double

55

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Schwanniomyces occidentalis*

(B) STRAIN: wild type

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 8..1390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GTCAATC	ATG	GTC	TCG	ATC	TCA	AAA	TTA	ATT	AAT	AAC	GGT	TTA	CTC	TTA	49	
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1					5					10						
GCT	GGT	CAA	AGT	GTT	TAC	CAA	GAT	TTA	GCT	ACT	CCA	CAA	CAA	TCT	TCC	97
Ala	Gly	Gln	Ser	Val	Tyr	Gln	Asp	Leu	Ala	Thr	Pro	Gln	Gln	Ser	Ser	
15					20					25					30	
GTC	GAG	CAG	TAT	AAT	ATT	ATT	AGG	TTT	TTA	GGT	GGT	TCG	GGT	CCT	TAC	145
Val	Glu	Gln	Tyr	Asn	Ile	Ile	Arg	Phe	Leu	Gly	Gly	Ser	Gly	Pro	Tyr	
				35					40					45		
ATT	CAA	CGC	AGT	GGT	TAT	GGT	ATT	TCC	ACT	GAT	ATT	CCT	GAT	CAG	TGC	193
Ile	Gln	Arg	Ser	Gly	Tyr	Gly	Ile	Ser	Thr	Asp	Ile	Pro	Asp	Gln	Cys	
			50					55				60				
ACA	ATT	AAG	CAA	GTT	CAG	TTG	ATG	TCA	AGG	CAT	GGG	GAA	AGA	TAC	CCT	241
Thr	Ile	Lys	Gln	Val	Gln	Leu	Met	Ser	Arg	His	Gly	Glu	Arg	Tyr	Pro	
		65				70						75				
TCA	AAA	AAC	TCT	GGT	AAG	AAG	TTA	AAA	ACA	ATA	TAT	GGT	AAA	TTA	AAG	289
Ser	Lys	Asn	Ser	Gly	Lys	Lys	Leu	Lys	Thr	Ile	Tyr	Gly	Lys	Leu	Lys	
	80					85					90					
AGC	TAC	AAT	GGC	ACT	TTC	ACA	GGT	AGC	TTA	GCT	TTT	TTG	AAT	GAC	TAT	337
Ser	Tyr	Asn	Gly	Thr	Phe	Thr	Gly	Ser	Leu	Ala	Phe	Leu	Asn	Asp	Tyr	
	95				100				105					110		
GAA	TAT	TTT	GTT	CCG	GAT	GAT	AGT	TTG	TAC	GAA	AAG	GAA	ACA	AGT	GCA	385
Glu	Tyr	Phe	Val	Pro	Asp	Asp	Ser	Leu	Tyr	Glu	Lys	Glu	Thr	Ser	Ala	
			115					120					125			
CTG	AAC	TCG	CAA	GGT	TTA	TTT	GCA	GGT	ACT	ACA	GAT	GCC	TTA	AGA	CAT	433
Leu	Asn	Ser	Gln	Gly	Leu	Phe	Ala	Gly	Thr	Thr	Asp	Ala	Leu	Arg	His	
			130					135					140			
GGT	GCT	GCT	TTT	AGA	GCT	AAA	TAT	GGA	TCA	TTG	TAT	AAA	CAA	AAT	TCT	481
Gly	Ala	Ala	Phe	Arg	Ala	Lys	Tyr	Gly	Ser	Leu	Tyr	Lys	Gln	Asn	Ser	
	145					150						155				
ACC	TTG	CCA	GTT	TTC	ACT	TCA	AAT	TCC	AAC	AGA	GTC	TAC	CAG	ACT	TCT	529
Thr	Leu	Pro	Val	Phe	Thr	Ser	Asn	Ser	Asn	Arg	Val	Tyr	Gln	Thr	Ser	
	160					165					170					

5	GAA TAC TTT GCC AGA GGT TTC TTA GGT GAT GAA TTT TCT GAT GCT ACT Glu Tyr Phe Ala Arg Gly Phe Leu Gly Asp Glu Phe Ser Asp Ala Thr 175 180 185 190	577
10	GTT CAC TTT GCT ATC ATT GAT GAA GAC CCT AAA ATG GGT GTT AAT TCA Val His Phe Ala Ile Ile Asp Glu Asp Pro Lys Met Gly Val Asn Ser 195 200 205	625
15	TTA ACA CCA AGA GCC GCT TGT GAC AAT TAT AAT GAG GAT GTG AAT GAC Leu Thr Pro Arg Ala Ala Cys Asp Asn Tyr Asn Glu Asp Val Asn Asp 210 215 220	673
20	GGC ATT GTC AAT CAA TAT AGC ACT GAC TAT TTG GAT GAA GCC CTT AAA Gly Ile Val Asn Gln Tyr Ser Thr Asp Tyr Leu Asp Glu Ala Leu Lys 225 230 235	721
25	AGA TTC CAA TCA TCA AAT CCA GGA TTG AAT TTG ACC TCG GAA GAC GTT Arg Phe Gln Ser Ser Asn Pro Gly Leu Asn Leu Thr Ser Glu Asp Val 240 245 250	769
30	TAC CAA CTT TTC GCT TAC TGT GCA TAT GAG ACT AAT GTT AAG GGT GCA Tyr Gln Leu Phe Ala Tyr Cys Ala Tyr Glu Thr Asn Val Lys Gly Ala 255 260 265 270	817
35	TCC CCA TTC TGT GAC TTA TTT ACT AAT GAA GAA TAC ATT CAA TAT TCC Ser Pro Phe Cys Asp Leu Phe Thr Asn Glu Glu Tyr Ile Gln Tyr Ser 275 280 285	865
40	TAC AGC GTT GAT CTT TCT AAT TAT TAT TCT CAC GGG GCA GGT CAT AAT Tyr Ser Val Asp Leu Ser Asn Tyr Tyr Ser His Gly Ala Gly His Asn 290 295 300	913
45	CTA ACT AAA ACC ATT GGT TCT ACT TTA TTA AAT GCC TCA TTA ACC TTA Leu Thr Lys Thr Ile Gly Ser Thr Leu Leu Asn Ala Ser Leu Thr Leu 305 310 315	961
50	TTA AAA GAT GGC ACC AAT GAC AAT AAA ATC TGG TTA TCT TTT TCA CAC Leu Lys Asp Gly Thr Asn Asp Asn Lys Ile Trp Leu Ser Phe Ser His 320 325 330	1009
55	GAT ACT GAT TTG GAA ATC TTC CAT AGT GCC TTA GGA ATT GTT GAG CCA Asp Thr Asp Leu Glu Ile Phe His Ser Ala Leu Gly Ile Val Glu Pro 335 340 345 350	1057
60	GCT GAA GAT TTA CCA GTT GAT TAC ATT CCT TTT CCA TCG CCA TAT ATT Ala Glu Asp Leu Pro Val Asp Tyr Ile Pro Phe Pro Ser Pro Tyr Ile 355 360 365	1105
65	CAC TCA CAA ATT GTT CCA CAA GGT GCT AGA ATT TAT ACT GAG AAA TAT His Ser Gln Ile Val Pro Gln Gly Ala Arg Ile Tyr Thr Glu Lys Tyr 370 375 380	1153
70	TCA TGT GGC AAC GAA ACC TAT GTT AGA TAT ATA CTT AAT GAT GCA GTT Ser Cys Gly Asn Glu Thr Tyr Val Arg Tyr Ile Leu Asn Asp Ala Val 385 390 395	1201
75	GTT CCA ATT CCA AAA TGC TCT TCT GGT CCA GGG TTC TCA TGT GAG CTT Val Pro Ile Pro Lys Cys Ser Ser Gly Pro Gly Phe Ser Cys Glu Leu 400 405 410	1249

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5 AGT AAA TTC GAA GAA TAT ATT AAT AAA AGA CTT AGG GAT GTT GAC TTT 1297
Ser Lys Phe Glu Glu Tyr Ile Asn Lys Arg Leu Arg Asp Val Asp Phe
415 420 425 430

GTT GAA CAA TGT GAT TTA AAA GAT GCT CCA ACT GAA GTT ACT TTT TAC 1345
Val Glu Gln Cys Asp Leu Lys Asp Ala Pro Thr Glu Val Thr Phe Tyr
435 440 445

10 TGG GAT TAC ACG TCG GTG AAC TAT AGT GCG TCC CTT ATT AAT GGT 1390
Trp Asp Tyr Thr Ser Val Asn Tyr Ser Ala Ser Leu Ile Asn Gly
450 455 460

TAAATTGAGT ATAGGAGAAT ATCTTATTTT TAGTTTGATC ACTATCTGAA TCCACTTTGC 1450

15 TCTTTCTCCT TGTTTTGATT GCTTATCCAT TGTTTAGAAA TAGGTTATAA AGCAATCATT 1510

TTTACAACATA TGTCGTCTAA TACTTTGTTT CTAGAATTAA AAAAAATAAT AGTATACCTG 1570

TGTAAAGTCT TACTTGATAG CTAAC TAGTC ACTTCTTAAT CATACACCTA ATCTATCCTA 1630

20 A 1631

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:
25 (A) LENGTH: 461 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

30 Met Val Ser Ile Ser Lys Leu Ile Asn Asn Gly Leu Leu Leu Ala Gly
1 5 10 15

Gln Ser Val Tyr Gln Asp Leu Ala Thr Pro Gln Gln Ser Ser Val Glu
20 25 30

35 Gln Tyr Asn Ile Ile Arg Phe Leu Gly Gly Ser Gly Pro Tyr Ile Gln
35 40 45

Arg Ser Gly Tyr Gly Ile Ser Thr Asp Ile Pro Asp Gln Cys Thr Ile
50 55 60

40 Lys Gln Val Gln Leu Met Ser Arg His Gly Glu Arg Tyr Pro Ser Lys
65 70 75 80

Asn Ser Gly Lys Lys Leu Lys Thr Ile Tyr Gly Lys Leu Lys Ser Tyr
85 90 95

45 Asn Gly Thr Phe Thr Gly Ser Leu Ala Phe Leu Asn Asp Tyr Glu Tyr
100 105 110

Phe Val Pro Asp Asp Ser Leu Tyr Glu Lys Glu Thr Ser Ala Leu Asn
115 120 125

50 Ser Gln Gly Leu Phe Ala Gly Thr Thr Asp Ala Leu Arg His Gly Ala
130 135 140

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5 Ala Phe Arg Ala Lys Tyr Gly Ser Leu Tyr Lys Gln Asn Ser Thr Leu
 145 150 155 160
 Pro Val Phe Thr Ser Asn Ser Asn Arg Val Tyr Gln Thr Ser Glu Tyr
 165 170 175
 Phe Ala Arg Gly Phe Leu Gly Asp Glu Phe Ser Asp Ala Thr Val His
 180 185 190
 10 Phe Ala Ile Ile Asp Glu Asp Pro Lys Met Gly Val Asn Ser Leu Thr
 195 200 205
 Pro Arg Ala Ala Cys Asp Asn Tyr Asn Glu Asp Val Asn Asp Gly Ile
 210 215 220
 15 Val Asn Gln Tyr Ser Thr Asp Tyr Leu Asp Glu Ala Leu Lys Arg Phe
 225 230 235 240
 Gln Ser Ser Asn Pro Gly Leu Asn Leu Thr Ser Glu Asp Val Tyr Gln
 245 250 255
 20 Leu Phe Ala Tyr Cys Ala Tyr Glu Thr Asn Val Lys Gly Ala Ser Pro
 260 265 270
 Phe Cys Asp Leu Phe Thr Asn Glu Glu Tyr Ile Gln Tyr Ser Tyr Ser
 275 280 285
 25 Val Asp Leu Ser Asn Tyr Tyr Ser His Gly Ala Gly His Asn Leu Thr
 290 295 300
 Lys Thr Ile Gly Ser Thr Leu Leu Asn Ala Ser Leu Thr Leu Leu Lys
 310 315 320
 30 Asp Gly Thr Asn Asp Asn Lys Ile Trp Leu Ser Phe Ser His Asp Thr
 325 330 335
 Asp Leu Glu Ile Phe His Ser Ala Leu Gly Ile Val Glu Pro Ala Glu
 340 345 350
 35 Asp Leu Pro Val Asp Tyr Ile Pro Phe Pro Ser Pro Tyr Ile His Ser
 355 360 365
 Gln Ile Val Pro Gln Gly Ala Arg Ile Tyr Thr Glu Lys Tyr Ser Cys
 370 375 380
 40 Gly Asn Glu Thr Tyr Val Arg Tyr Ile Leu Asn Asp Ala Val Val Pro
 385 390 395 400
 Ile Pro Lys Cys Ser Ser Gly Pro Gly Phe Ser Cys Glu Leu Ser Lys
 405 410 415
 45 Phe Glu Glu Tyr Ile Asn Lys Arg Leu Arg Asp Val Asp Phe Val Glu
 420 425 430
 Gln Cys Asp Leu Lys Asp Ala Pro Thr Glu Val Thr Phe Tyr Trp Asp
 435 440 445
 50 Tyr Thr Ser Val Asn Tyr Ser Ala Ser Leu Ile Asn Gly
 450 455 460

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Claims

1. A phytase consisting essentially of a single type of subunits, which can hydrolyze a phytate to *myo*-inositol.
- 5 2. The phytase according to claim 1, which has a residual activity of not less than 90% after heat treatment at 70°C for 30 minutes.
3. The phytase according to claim 1 or 2, wherein said subunit has a molecular size after removing sugar chains of $50 \text{ kD} \pm 5 \text{ kD}$ determined by SDS-polyacrylamide gel electrophoresis.
- 10 4. The phytase according to claim 1, which is originated from a microorganism, preferably from a yeast.
5. The phytase according to claim 4, wherein said yeast is one belonging to genus *Schwanniomyces*, and preferably is *Schwanniomyces occidentalis*.
- 15 6. The phytase according to claim 5, which is produced by culturing *Schwanniomyces occidentalis* under conditions inducing production of said phytase.
7. The phytase according to claim 6, wherein *Schwanniomyces occidentalis* is cultured in a culture medium containing calcium salt of a weak acid, preferably CaCO_3 , and a low concentration of phosphate source.
- 20 8. The phytase according to claim 7, wherein said concentration of said phosphate source is 1 to 6000 mg/l.
9. The phytase according to claim 8, wherein said culture medium contains a phytate as a sole phosphate source.
- 25 10. The phytase according to any of the claims 1 to 9, which contains the amino acid sequence shown in SEQ ID NO. 1 and/or SEQ ID NO. 2.
11. The phytase according to claim 10, which contains the amino acid sequence shown in SEQ ID NO. 5.
- 30 12. A cloned gene originated from *Schwanniomyces occidentalis*, which encodes a phytase subunit having a molecular size after removing sugar chains of $50 \text{ kD} \pm 5 \text{ kD}$ determined by SDS-polyacrylamide gel electrophoresis.
13. The gene according to claim 12, which encodes the amino acid sequence shown in SEQ ID NO. 5.
- 35 14. The gene according to claim 12, which contains at least one DNA sequence having a nucleotide sequence shown in SEQ ID NO. 3, SEQ ID NO. 4 or SEQ ID NO. 5.
15. The gene according to claim 14, which has the nucleotide sequence shown in SEQ ID NO. 5.
- 40 16. A recombinant vector containing the gene according to any of the claims 12 to 15, wherein said recombinant vector can express said gene in a host cell.
17. The recombinant vector according to claim 16, which is YE pGPH1.
- 45 18. A microorganism transformed with said recombinant vector according to claim 16 or claim 17.
19. The microorganism according to claim 18, which is *Escherichia coli*, preferably *Escherichia coli* FERM BP-5108.
- 50 20. The microorganism according to claim 18, which is a yeast, preferably *Saccharomyces cerevisiae* FERM BP-5109.
21. Treated cells of said microorganism according to claim 18.
22. A process for producing a phytase according to any of the claims 1 to 3 by culturing a microorganism according to any of the claims 18 to 20 and isolating the phytase from the culture medium.
- 55 23. A method for converting a phytate into *myo*-inositol comprising contacting the phytate with the phytase according to any of the claims 1 to 3.

24. The method according to claim 23, wherein said phytate is treated with cells or treated cells or a culture medium containing the cells of said microorganism according to any of the claims 18 to 21.

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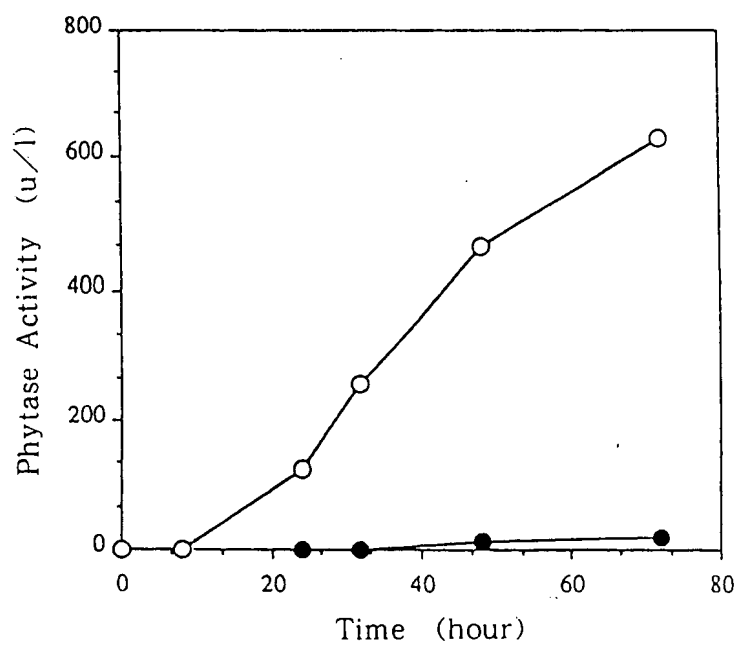


Fig. 1

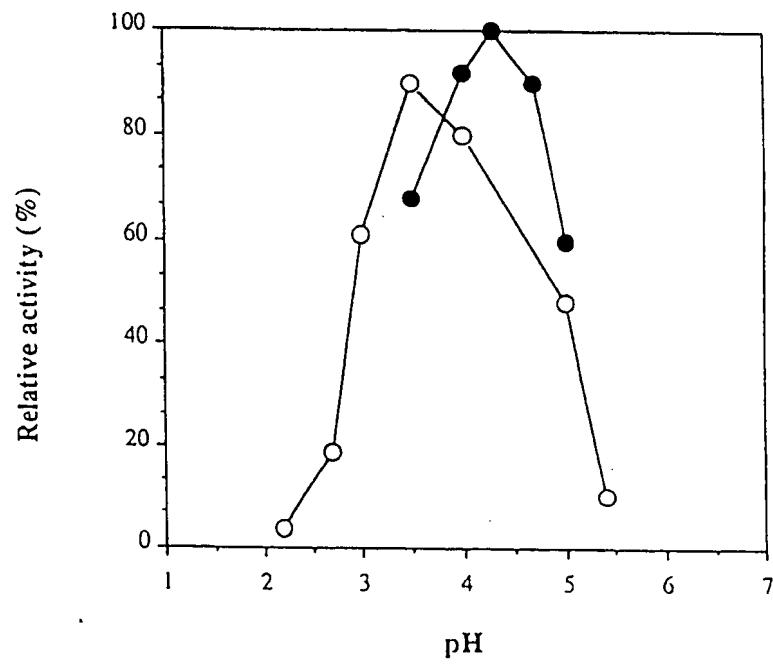


Fig. 2

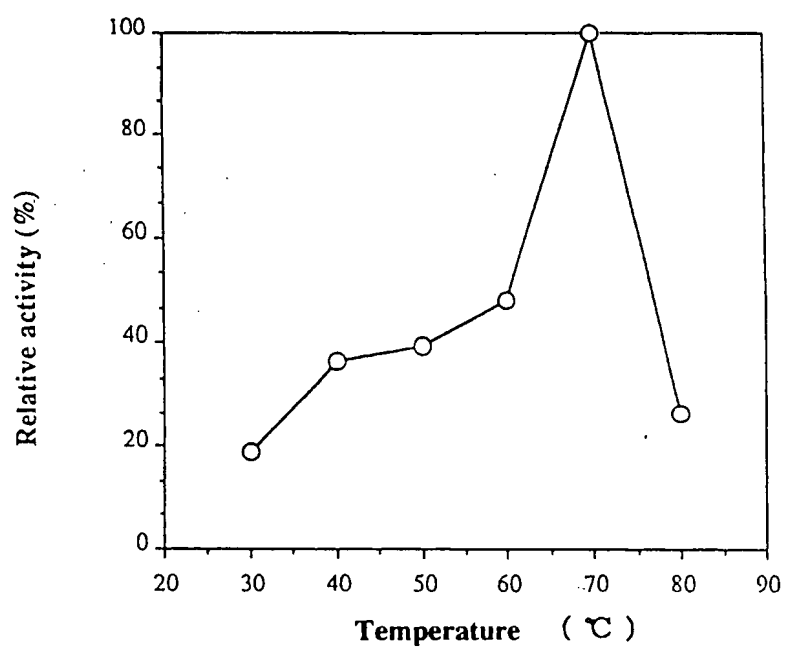


Fig. 3

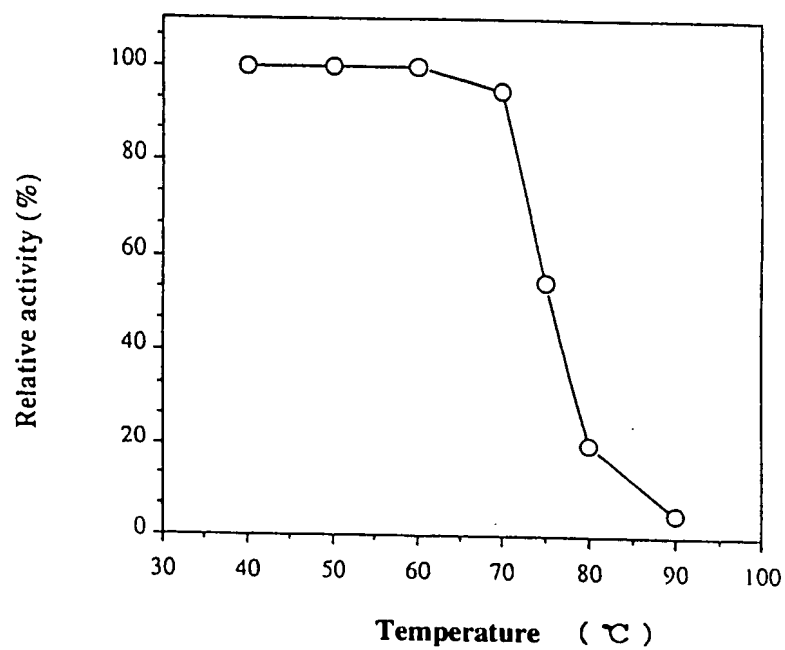


Fig. 4

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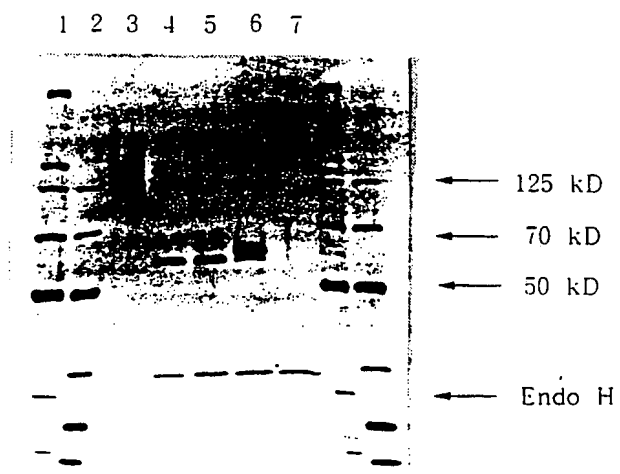


Fig. 5

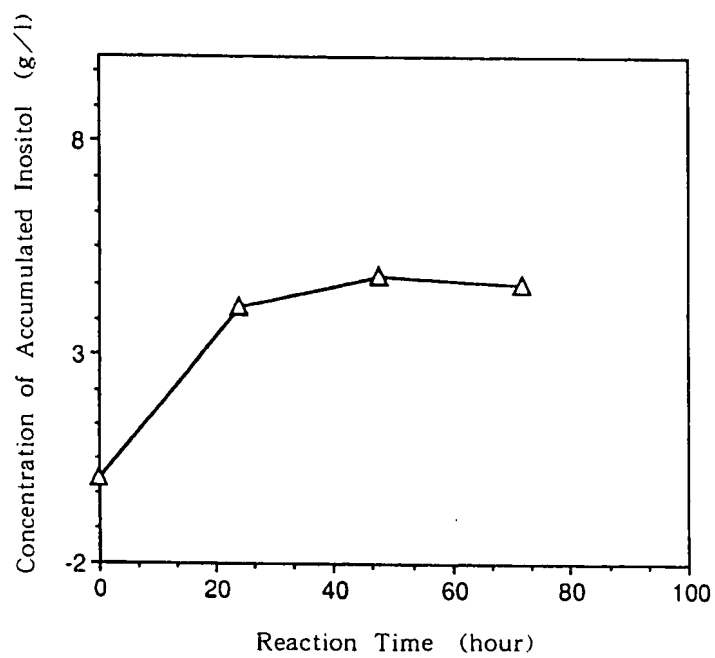


Fig. 6

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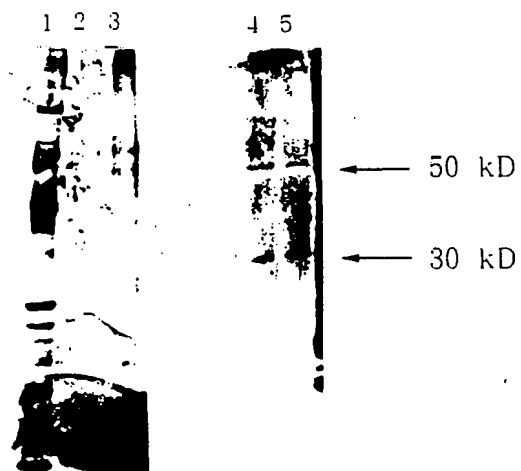


Fig. 7

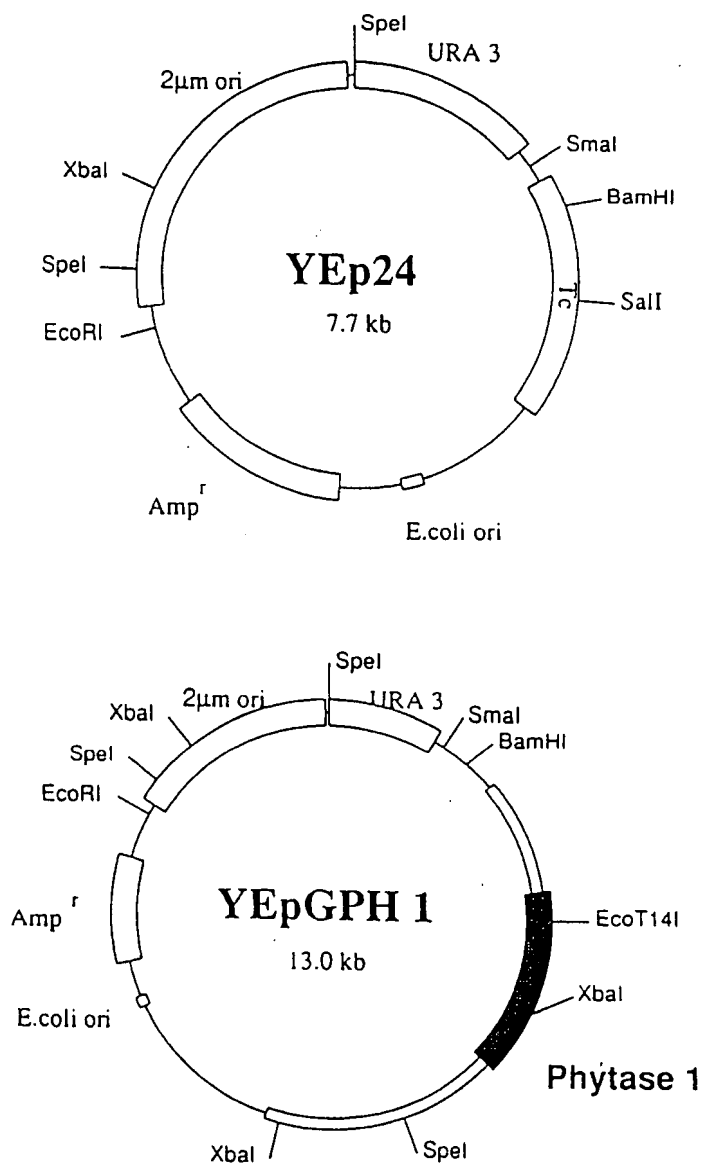


Fig. 8

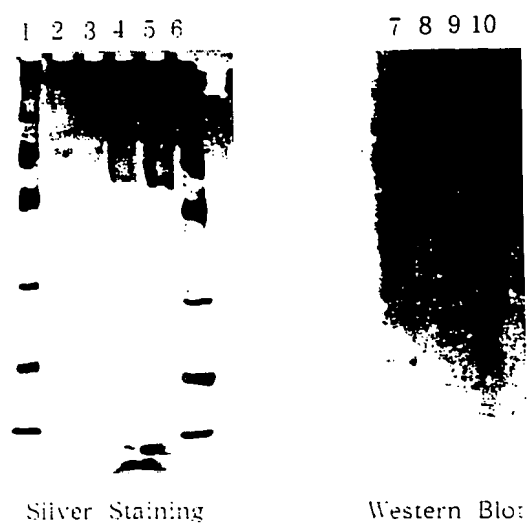
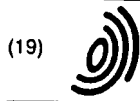


Fig. 9



(19)

Europäisches Patentamt

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(11)

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(12)

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C12N 15/70, C12N 1/21,
C12N 1/19, C12P 7/18
// (C12N1/21, C12R1:19),
(C12N1/19, C12R1:865)

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24.02.1995 JP 60111/95

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(54) Novel Phytase

(57) A novel phytase is disclosed. The phytase consists essentially of a single type of subunits, and can hydrolyze a phytate to *myo*-inositol. A gene encoding the phytase, which is originated from *Schwanniomyces occidentalis* is also disclosed.

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European Patent
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EUROPEAN SEARCH REPORT

Application Number
EP 95 11 0503

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X	WO 94 03072 A (PANLABS INC ;NEVALAINEN HELENA K M (AU); ALKO LTD (FI); PALOHEIMO) 17 February 1994 * page 17, paragraph 2 * * page 33; figure 9 *	1,3,4,23	/(C12N1/21, C12R1:19), (C12N1/19, C12R1:865)
X	EP 0 420 358 A (GIST BROCADES NV) 3 April 1991 * page 7; table 1 *	1,3,4,23	
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A	SEGUEILHA L. ET AL.: "Purification and properties of the phytase from <i>Schwanniomyces castellii</i> " JOURNAL OF FERMENTATION AND BIOENGINEERING, vol. 74, no. 1, 1992, pages 7-11. XP002053183 * page 9 - page 11 *	1-9,23	
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The present search report has been drawn up for all claims			
Place of search THE HAGUE		Date of completion of the search 30 January 1998	Examiner Macchia, G
<p>CATEGORY OF CITED DOCUMENTS</p> <p>X particularly relevant if taken alone / particularly relevant if combined with another document of the same category A technological background O non-written disclosure P intermediate document</p> <p>T theory or principle underlying the invention E earlier patent document, but published on, or after the filing date D document cited in the application L document cited for other reasons S member of the same patent family, corresponding document</p>			

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

European Patent
Office

EUROPEAN SEARCH REPORT

Application Number
EP 95 11 0503

DOCUMENTS CONSIDERED TO BE RELEVANT			
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (Int.Cl.6)
A	SEGUEILHA L. ET AL.: "Reduction of phytate content in wheat bran and glandless cotton flour by Schwanniomyces castellii" JOURNAL OF AGRICULTURAL AND FOOD CHEMISTRY. vol. 41, no. 12, December 1993, pages 2451-2454, XP002053184 * the whole document *	5-9	
A	NAYINI N.R. AND MARKAKIS P.: "The phytase of yeast" LEBENSMITTEL WISSENSCHAFT UND TECHNOLOGIE. vol. 17, no. 1, 1984, pages 24-26, XP002054007 * abstract * * page 26, right-hand column *	1,4	
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The present search report has been drawn up for all claims			
Place of search THE HAGUE		Date of completion of the search 30 January 1998	Examiner Macchia, G
CATEGORY OF CITED DOCUMENTS X particularly relevant if taken alone Y particularly relevant if combined with another document of the same category A technological background O non-written disclosure P intermediate document T theory or principle underlying the invention E earlier patent document, but published on, or after the filing date D document cited in the application L document cited for other reasons S member of the same patent family corresponding document			

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